

# Benedict N. Anchang, PhD

## Personal Data

Address: 2609 Azalea Dr, Durham, 27703, NC, USA  
Email: [benedict.anchang@nih.gov](mailto:benedict.anchang@nih.gov)  
TEL: 984-287-3350  
eFAX: [benedict.anchang%4802455@fax.nih.gov](mailto:benedict.anchang%4802455@fax.nih.gov)  
FAX: 301-480-2455  
Website: <https://www.niehs.nih.gov/research/atniehs/labs/bb/staff/anchang/index.cfm>

## Academic Positions

Aug 2019 –	Position	Stadtman Investigator: NIH/NIEHS/NCI National Institute of Environmental Health Sciences Biostatistics and Computational Biology Branch PO Box 12233 111 TW Alexander Drive Bldg 101 / Mail Drop A3-03 Research Triangle Park, NC 27709-2233
Jan 2017 – Aug 2019	Position:	Instructor
	Department:	Radiology & Biomedical Data Science Integrative Biomedical Imaging Stanford University, School of Medicine, James H. Clark Center, Room S255 318 Campus Drive West Stanford, CA 94305

## Administrative Appointments

Oct 2017 – Aug 2019	Position:	Chair for Diversity Trainee Subcommittee, Radiology Department
	Website:	<a href="https://web.stanford.edu/dept/radiology/cgi-bin/raddiversity/">https://web.stanford.edu/dept/radiology/cgi-bin/raddiversity/</a>

## Awards, Honors, Fellowships

1. NIH **Distinguished Scholar Program** award, 2019
2. Grant on Collaborative Computational Tools for the Human Cell Atlas project, **Chan Zuckerberg Initiative DAF** (2018 - 2019)

3. **Best oral presentation** International Conference on Intelligent Systems for Molecular Biology /European Conference on Computational Biology (**ISMB/ECCB**), **TransMed Proceedings**, Basel Switzerland, July 2019
4. **American Association for Cancer Research** (AACR) Minority and/or Minority-Serving Institution Faculty Scholar in **Cancer Research Award** (2018)
5. 2018 **Delegate for BD2K NIH sponsored Data Science Innovation Lab**: Mathematical Challenges of Single Cell Dynamics
6. **Certification award** on **College Science Teaching and STEM**, University of Michigan (2016)
7. **Travel fellowship** for International Conference on Intelligent Systems for Molecular Biology (**ISMB**) international conference in Boston, USA (July 2010)
8. **Travel fellowship** for **International Society of Computational Biology** (ISCB) international conference in Bamako, Mali (December 2009)
9. **Postdoctoral Scholar Certificate**, **Stanford University** (2016)
10. Bio-X Corporate Forum Liaison sponsorship to attend the PMWC 2014 World Conference on Personalized Medicine 2014 in Silicon Valley

## Patent Applications

1. **Anchang Benedict & Sylvia K. Plevritis** (2017). Systems and Methods for Targeted Therapy Based on Single-Cell Stimulus Perturbation Response. **Patent PCT/US2017/026243**, 12/10/2017.

## Education

June 2007 - Dec 2011	<p>Certificate: Ph.D. in Bioinformatics</p> <p>University: University of Regensburg, Germany</p> <p>Thesis title: <i>“Modeling the interplay of molecular signaling and gene expression using dynamic nested effects models”</i></p> <p>Advisors: Prof Rainer Spang (Co-advisor Prof Gronwald Wolfram)</p>
Oct 2005 - Nov 2006	<p>Certificate: Master of Science in Biostatistics</p> <p>University: University of Hasselt, Diepenbeek, Belgium</p> <p>Thesis title: <i>“Age profiles of campylobacter seroprevalence from hierarchical distribution mixtures”</i></p> <p>Advisors: Prof Ziv Shkedy, Dr Peter Teunis, Dr Harriet Namata</p>

Oct 2004 - Sept 2005	Certificate:	Master of Science in Applied Statistics
	University:	Limburgs Center for Statistics, Diepenbeek, Belgium
	Thesis title:	<i>“Determination of critical values of oscillatory gas exchange parameters during exercise in healthy children using mixed effects models”</i>
	Advisors:	Prof Hebert Thijs and Prof Geert Molenberghs
Oct 1998 - July 2002	Certificate:	Bachelor of Science in Mathematics and Computer Science
	University:	University of Buea, Cameroon

## Research and Teaching Experience

Aug 2019 -	<b>Institution</b>	NIH/NIEHS/NCI
	<b>Research</b>	<ul style="list-style-type: none"> <li>• Develop methods for visualizing and modelling temporal and spatial high-dimensional single-cell data</li> <li>• Develop methods for integration of molecular and pathological features to differentiate between chemically-induced, adverse biological processes associated with neoplastic and non-neoplastic lesions</li> </ul>
Jan 2017 – Aug 2019	<b>Institution:</b>	Stanford University
<b>Instructor</b>	<b>Research:</b>	<ul style="list-style-type: none"> <li>• Develop computational models to visualize, improve our understanding of normal and disease progression to help target the complex tumor microenvironment using high-dimensional single-cell data</li> <li>• PI on Chan Zuckerberg Initiative grant entitled <i>“Detection and Visualization of Temporal Partitioned Cellular States using Single-cell Analysis”</i> with main focus on EMT in lung cancer.</li> <li>• Co-Investigator for the NIH U54-CA209971 Center grant on Modeling the Role of Lymph Node Metastasis in Tumor-Mediated Immunosuppression.</li> <li>• Co-Investigator for the NIH 1U54HG010426-01 Center grant to map the complexity of cellular</li> </ul>

		architecture and biomolecular profiles of the small bowel and colon (NIH HuBMAP project)
	<b>Teaching:</b>	<ul style="list-style-type: none"> <li>• Single cell RNA-seq analysis lecture (<b>CBIO243</b>) for undergraduate and graduate cancer biology trainees.</li> </ul>
Feb 2012 - Sep 2016	<b>Institution:</b>	Stanford University, Center for Cancer Systems Biology, <b>Sylvia Plevritis lab</b>
<b>Postdoctoral Scholar Computational Biology</b>	<b>Projects:</b>	<ul style="list-style-type: none"> <li>• Develop algorithms for analyzing high throughput single cell drug screening data with the ultimate goal of achieving better-individualized combination therapy by accounting for intratumor heterogeneity.</li> <li>• Develop computational tools for sorting and analyzing single cell fluorescence and mass cytometry data.</li> <li>• Develop computational tools for the analysis of oncogenic survival mechanisms related to biological processes like senescence and innate immunity based on high content genomic data</li> </ul>
June 2007 - Dec 2011	<b>Institution:</b>	Institute of Functional Genetics and Bioinformatics, Regensburg, Germany
<b>PhD Candidate Research Assistant</b>	<b>Projects:</b>	<ul style="list-style-type: none"> <li>• Modeling the dynamics of signaling and gene expression using high throughput genomic data</li> <li>• Develop and apply methodology called Dynamic Nested Effects Models</li> <li>• Network reconstruction on Wnt signaling pathway using <b>next generation RNAi</b> sequencing data from colon cancer cell lines</li> </ul>
July 2006 - Sep 2006	<b>Institution:</b>	• National Institute of Public Health and Environment Netherlands
<b>Summer Intern</b>	<b>Function:</b>	Data Analysis <ul style="list-style-type: none"> <li>• Analyzed data and wrote a report on age profiles on campylobacter seroprevalence in the Netherlands</li> </ul>

## Research Interests / Methods & Techniques

Systems biomedicine, Cancer Systems Biology, Translational Systems Biology, Single-cell analysis, Trajectory modeling, Mixtures, Toxicology, Immunology, Neuroscience, Synthetic biology, Drug combination optimization, biomarker discovery, neural networks, deep learning, dynamic and spatial inference, causal inference and modeling of biological networks, integration of genomic and clinical data, clinical informatics, Data Reduction and high-dimensional multi-scale modeling.

## Publications

1. Karacosta, L.G., Anchang, B., Ignatiadis, N. *et al.* Mapping lung cancer epithelial-mesenchymal transition states and trajectories with single-cell resolution. *Nat Commun* **10**, 5587 (2019) doi:10.1038/s41467-019-13441-6
2. **Anchang B**, Kara Davis, Brian Williamson, Harris Fienberg, Loukia Karacosta, Sean C Bendall, Robert Tibshirani, Garry Nolan and Sylvia K Plevritis. (2018). DRUG-NEM: Optimizing drug combinations using single-cell perturbation response to account for intratumoral heterogeneity. *Proceedings of the National Academy of Sciences* 2018; 115 (18): E4294–E4303.
3. Michael Patrick Menden, Dennis Wang, Yuanfang Guan, Michael Mason, Bence Szalai, Krishna C Bulusu, Thomas Yu, Jaewoo Kang, Minji Jeon, Russ Wolfinger, Tin Nguyen, Mikhail Zaslavskiy, et al., **AstraZeneca-Sanger Drug Combination DREAM Consortium**. Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen *Nature Communications*, **10** : 2674 (2019).
4. **Anchang B**, Tom DP Hart, Sean C Bendall, Peng Qiu, Zach Bjornson, Michael Linderman, Gary Nolan, and Sylvia Plevritis. (2016). Visualization and cellular hierarchy inference of single-cell data using SPADE. *Nature Protocols*, 11, 1264–1279.
5. Yan, K., Gevaert, O., Zheng, G., **Anchang, B.** et al. (2017). Intestinal Enteroendocrine Lineage Cells Possess Homeostatic and Injury-Inducible Stem Cell Activity. *Cell Stem Cell* 21(1):78- 90.e6
6. **Anchang, B.**, Do, M.T., Zhao, X., Plevritis S.K. (2014). CCAST: A model-based gating strategy to isolate homogeneous subpopulations in heterogeneous population of single cells. *Plos Computational Biology*, 10(7): e1003664.
7. Dumcke, S., Brauer J., **Anchang, B.**, Spang R., Beerenwinkel, N., Tresch A. (2014). Exact likelihood computation in Boolean networks with probabilistic time delays, and its application in signal network reconstruction. *Bioinformatics*, 30(3): 414-9
8. **Anchang, B.**, Sadeh M., Jacob, J., Tresch, A., Vlad, O.M., Oefner, P., Spang R. (2009). Modeling the temporal interplay of molecular signaling and gene expression by using dynamic nested effects models. *Proceedings of the National Academy of Sciences*, 106(16): 6447 - 6452.

9. Oksana Voloshanenko, Gerrit Erdmann, Taronish D. Dubash, Iris Augustin, Marie Metzgi, Giusi Moffa, Christian Hundsruker, Grainne Kerr, Thomas Sandmann, **Benedict Anchang**, Kubilay Demir, Christina Boehm, Svenja Leible, Claudia R. Ball, Hanno Glimm, Rainer Spang and Michael Boutros. (2013). Wnt secretion is required to maintain canonical Wnt signaling in colon cancer cell lines. *Nature Communications*, 4:2610
10. Alper Yetil, **Benedict Anchang** Arvin Guow, Stacey J. Adam, Tahera Zabuawala, Ramya Parameswaran, Jan van Riggelen Sylvia Plevritis and Dean W. Felsher. (2015). p19ARF is a critical mediator of cellular senescence and the innate immune response associated with MYC suppression in acute leukemia. *Oncotarget*, 6(6), 3563-3577.
11. Kearney AY, **Anchang B**, Plevritis S, Felsher DW. ARF: Connecting senescence and innate immunity for clearance. *Aging* (Albany NY). 2015 Sep 25; PubMed PMID: 26412380.
12. **Anchang B**, Harris Fienberg, Sean Bendall, Robert Tibshirani, Sylvia K. Plevritis. Multi-target drug combinations from single drug responses measured at the level of single cells using Mixture Nested Effects Models (MNEMs) applied to cancer. In: *Proceedings of the American Association for Cancer Research (AACR) Special Conference on Computational and Systems Biology of Cancer*; Feb 8-11, 2015; San Francisco, CA. Philadelphia (PA): AACR; Cancer Res 2015; 75 (22 Suppl 2): Abstract nr B1-39.
13. **Anchang, B** (2011). Modeling molecular signaling and gene expression using Dynamic Nested Effects Models. PhD, Universität Regensburg. [urn:nbn:de:bvb:355-epub-229962](https://nbn-resolving.org/urn:nbn:de:bvb:355-epub-229962)
14. **Anchang, B et al. (2010)**. Modeling the temporal interplay of molecular signaling and gene expression by using dynamic nested effects models. *Highlight track proceedings* of the 18<sup>th</sup> Annual International Conference on intelligent Systems for Molecular Biology (ISMB), Boston, USA.
15. **Ameen A. Salahudeen, Junjie Zhu, Anchang Benedict et al. 2018**. Organoid-based characterization of distal adult human lung at single cell resolution. **Preparation for resubmission to Nature.**

## Mentoring, Outreach and Leadership Activities

1. Promote Diversity in the department of Radiology by: increasing awareness within the Stanford community using surveys and publishing monthly newsletters on diversity, helping to attract and recruit new trainees, organizing social events and inviting guest speakers who promote diversity e.g. Hannah Valentine, MD (NIH Chief Officer for Scientific Workforce Diversity).
2. PI on a project funded by Silicon Valley Community Foundation in support of Chan Zuckerberg Initiative (CZI)

3. Participated in a project highlighting the critical contributions of Bay Area immigrants to the social, cultural, and economic betterment of America initiated by an international freelance photographer Mark Tuschman (<http://tuschmanphoto.com>).
4. Key participant in the Pilot Postdoctoral Mentoring program between Novartis Institutes for Biomedical Research (**NIBR**) and Stanford Bio-X (2016)
5. Supervising computational projects for young scholars in the Cancer Systems Biology Scholar Program (CSBS), Stanford University (2016-present)
6. Participated in the certified STEM and diversity Teaching and mentoring postdoctoral program at Stanford (Summer 2016)
7. Wrote a peer reviewed and scored NIH Research Scientist Development K01 Award application, which involved bringing together a team of mentors and collaborators (2015-2016).
8. Participated as a delegate in a 5-day intensive BD2K NIH sponsored Data Science Innovation Lab: Mathematical Challenges of Single Cell Dynamics in Oregon (2018) which resulted in bringing investigators with diverse expertise from different universities to work on particular project proposals with funding potential. This effort is still ongoing.
9. Planning committee member and Chair of the discussion session on “Mechanisms of Acquired Resistance in cancer” during the Integrative Cancer Biology Program (ICBP) Junior Investigator Meeting, November 13-15, 2013, Bethesda
10. Supervised NCI ICBP Summer Intent Student 2013, Brian Williamson (Undergraduate) at Stanford University. Now a graduate student studying Biostatistics at Washington State University.
11. Supervised NCI ICBP Summer Intent Student 2014, Tom Hart (Undergraduate) at Stanford University. Now a graduate student studying at Rockefeller University

## Meetings and Presentations

### Oral Presentations

1. Combining machine learning and single-cell analysis for individualize precision medicine. 22<sup>nd</sup> Annual ISMB/EECCB meeting, Basel, Switzerland, July 22, 2019
2. Loukia Karacosta, Benedict Anchang et al. 2018. AACR Annual Meeting, Chicago Illinois.  
**Presentation** on Identifying Dynamic EMT Transition States and Constructing a Proteomic EMT Landscape of Lung Cancer Using Single Cell Multidimensional Analysis.

2. Inaugural meeting for Systems Approaches to Cancer Biology sponsored by Association of Early Career Cancer Systems Biology and National Cancer Institute of the National Institute of Health, Woods Hole, MA, USA. April 3-6, 2016. **Presentation** on DRUG-NEM: an optimized drug combination strategy using single-cell perturbation response that accounts for intratumoral heterogeneity.
3. **Anchang et. al.** 2016. Short presentation on precision medicine using single-cell perturbation analysis during the inaugural Artificial Intelligence in Medicine (AI Med) meeting at the Ritz Carlton in Laguna Niguel, CA (December 12-15, 2016).
4. **NCI ICBP Mathematical Modeling of Cancer Systems Meeting.** CCAST: A model-based gating strategy to isolate homogeneous subpopulations in heterogeneous population of single cells, Tampa, Florida, February 26-28, 2015
5. 9<sup>th</sup> **European Conference on Computational Biology (ECCB)** Ghent, Belgium-September 26-29<sup>th</sup> 2010. **Workshop presentation:** Learning from perturbation effects.
6. 18<sup>th</sup> Annual **ISMB conference**, Boston, USA, July 13, 2010. **Highlight track presentation** on dynamic modeling of cellular decision-making. Video: [http://www.iscb.org/cms\\_addon/multimedia/flvmedia.php?i=698](http://www.iscb.org/cms_addon/multimedia/flvmedia.php?i=698)
7. 5<sup>th</sup> **RECOMB Conference on Regulatory and Systems Genomics, with DREAM Challenges** San Francisco, USA, November 12-15, 2012. **Systems Biology Session presentation** on “A non-parametric model-based framework to quantify heterogeneous populations in fluorescence activated cell sorting data”. Video: <https://www.iscb.org/recomb-mm/media-recombrsg2012>
8. 22<sup>nd</sup> Annual **ISMB conference**, Boston, USA, July 13, 2014. **Short presentation** on DRUGMNEM: an optimization strategy for targeted combination of drugs using single-drug screening single cell data
9. **ISCB International Conference on Bioinformatics** Bamako, Mali December 1-4th 2009. **Presentation** on dynamic nested effects models.
10. Bioinformatics seminar at the Schleusenwerterhaus Regensburg, Germany, June 19, 2009.

### **Peer reviewed Abstract and Poster Presentations**

1. Combining machine learning and single-cell analysis for individualize precision medicine. 22nd Annual ISMB/EECCB meeting, Basel, Switzerland, July 22, 2019.
2. Anchang et al. 2018. AACR Annual Meeting, Chicago Illinois. Presentation on Individualized drug combination based on single-cell drug perturbations.
3. Anchang et al. 2015 AACR Translation of the Cancer Genome and Computational and Systems Biology Conferences. Presentation on Multi-target drug combinations from single drug



responses measured at the level of single cells using Mixture Nested Effects Models (MNEMs) applied to cancer. 7-11 February 2015, San Francisco, CA, USA.

3. Daniel Koch, Stacey Adams, Andrew Gentles, **Benedict Anchang**, Delaney Sullivan, Sylvia Plevritis, Dean Felsher. Gene expression signatures associated with MYC oncogene addiction in lymphoma. **abstract**. In: Proceedings of the **AACR** Special Conference on Myc: From Biology to Therapy; Jan 7-10, 2015; La Jolla, CA. Philadelphia (PA): AACR; Mol Cancer Res 2015; 13(10 Suppl): Abstract nr A48.
4. 22<sup>nd</sup> Annual International Conference on intelligent Systems for Molecular Biology (ISMB), Boston, USA, July 13, 2014. **Presentation** on DRUGMNEM: an optimization strategy for targeted combination of drugs using single-drug screening single cell data
5. Keystone Symposia on Molecular and Cellular Biology: Engineering Cell Fate and Function,
  - a. Olympic Valley, California, USA, April 6-11, 2014. **Presentation** on “An optimal gating
  - b. strategy isolates homogeneous cell subpopulations in heterogeneous single cell data”
6. 18<sup>th</sup> Annual International Conference on intelligent Systems for Molecular Biology (ISMB), Boston, USA, July 13, 2010. **Presentation** on dynamic modeling of cellular decision-making.
7. 5<sup>th</sup> RECOMB Conference on Regulatory and Systems Genomics, with DREAM Challenges San Francisco, USA, November 12-15, 2012. **Presentation** on “A non-parametric model-based framework to quantify heterogeneous populations in fluorescence activated cell sorting data”.
8. Cell Symposia: Hallmarks of Cancer Meeting, San Francisco, USA, October 29-31, 2012. **Presentation** on Maintenance of Cellular Phenotypes in Breast Cancer Cell Lines from Sorted Cells.
9. CCSB EAB/NCI site meeting Stanford, USA. October 22, 2012. **Presentation** on “A Non-parametric Model-based Framework to identify and quantify Heterogeneous populations in FACS Data”.
10. ISCB International Conference on Bioinformatics Bamako, Mali December 1-4<sup>th</sup> 2009. **Presentation** on dynamic nested effects models.
11. Anchang et al. 2009. **IEEE** International Conference on Bioinformatics and Biomedicine Workshop Bethesda, MD, USA, November 1-4<sup>th</sup> 2009. **Presentation** on Modeling the Temporal Interplay of Molecular Signaling and Gene Expression by using Dynamic Nested Effects Models

## Professional Memberships and Other activities

1. ISCB member since 2009

2. AACR member since 2015
3. MICR member since 2018
4. Participated in the AstraZeneca-Sanger Drug Combination DREAM Challenge 2015
5. Reviewed submitted computational papers in Bioinformatics, PNAS, Plos Computational Biology ,RNA Biology and Plos one
6. Part of the ApoNET project (2007-2011) - Systems Analysis of Death Receptor Signaling Networks. <http://www.erasysbio.net/index.php?index=273>
7. Alumni member in A2B2D (Biostatistics-Bioinformatics) Diepenbeek, Belgium. 2006-present

## IT Skills

<b>Environments:</b>	Windows, Linux, Mac
<b>Languages:</b>	<b>R, S-plus, Python</b>
<b>Implemented software:</b>	<p>Author of the <b>R statistical package dnem</b>: dynamic nested effects models.</p> <p>Author of <b>SPADE-Forest R package</b>: Single-cell visualization</p> <p>Author of the <b>R package CCAST</b>: Clustering, Classification and Sorting Tree</p> <p>Author of the <b>R package PHENotypic STate MaP PHENOSTAMP</b></p> <p>Author of the <b>R package DRUGNEM</b>: Drug Nested Effects Models</p> <p>Collaborative Tools in R for the Chan Zuckerberg Initiative</p> <p>Human Cell Atlas project using <b>GitHub, Jupyter Notebook</b>.</p>
<b>Others</b>	Winbugs, SAS, Bioconductor, GitHub, Cytobank, LINCS, CCLE, Connectivity map, GO, KEGG, Twilight, ToppGene, GSEA, DAVID, etc.
<b>Text Processing:</b>	Latex, MS Office

## Languages

<b>English:</b>	Mother Tongue
<b>French:</b>	Good both in speaking and writing
<b>German:</b>	Fair both in speaking and writing
<b>Dutch:</b>	Beginner